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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/254,344

DATE: 04/30/2001
 TIME: 13:26:48

Input Set : A:\024705-077.ST25.txt
 Output Set: N:\CRF3\04302001\I254344.raw

ENTERED

4 <110> APPLICANT: HAYASHIZAKI, Yoshihide
 5 WATAHIKI, Masanori
 7 <120> TITLE OF INVENTION: RNA Polymerase
 9 <130> FILE REFERENCE: 024705-077
 11 <140> CURRENT APPLICATION NUMBER: US 09/254,344
 12 <141> CURRENT FILING DATE: 1999-09-03
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03037
 15 <151> PRIOR FILING DATE: 1998-07-06
 17 <150> PRIOR APPLICATION NUMBER: JP 9/180883
 18 <151> PRIOR FILING DATE: 1997-07-07
 20 <150> PRIOR APPLICATION NUMBER: JP 10/155759
 21 <151> PRIOR FILING DATE: 1998-06-04
 23 <160> NUMBER OF SEQ ID NOS: 23
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2659
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Bacteriophage T7
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (10)..(2658)
 36 <400> SEQUENCE: 1
 37 aggcactaa atg aac acg att aac atc gct aag aac gac ttc tct gac atc 51
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 39 1 5 10
 41 gaa ctg gct gct atc ccg ttc aac act ctg gct gac cat tac ggt gag 99
 42 Glu Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu
 43 15 20 25 30
 45 cgt tta gct cgc gaa cag ttg gcc ctt gag cat gag tct tac gag atg 147
 46 Arg Leu Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met
 47 35 40 45
 49 ggt gaa gca cgc ttc cgc aag atg ttt gag cgt caa ctt aaa gct ggt 195
 50 Gly Glu Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly
 51 50 55 60
 53 gag gtt gcg gat aac gct gcc gcc aag cct ctc atc act acc cta ctc 243
 54 Glu Val Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu
 55 65 70 75
 57 cct aag atg att gca cgc atc aac gac tgg ttt gag gaa gtg aaa gct 291
 58 Pro Lys Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala
 59 80 85 90
 61 aag cgc ggc aag cgc ccg aca gcc ttc cag ttc ctg caa gaa atc aag 339
 62 Lys Arg Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys
 63 95 100 105 110
 65 ccg gaa gcc gta gcg tac atc acc att aag acc act ctg gct tgc cta 387
 66 Pro Glu Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu
 67 115 120 125
 69 acc agt gct gac aat aca acc gtt cag gct gta gca agc gca atc ggt 435

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70 Thr Ser Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly
71          130          135          140
73 cgg gcc att gag gac gag gct cgc ttc ggt cgt atc cgt gac ctt gaa      483
74 Arg Ala Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu
75          145          150          155
77 gct aag cac ttc aag aaa aac gtt gag gaa caa ctc aac aag cgc gta      531
78 Ala Lys His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val
79          160          165          170
81 ggg cac gtc tac aag aaa gca ttt atg caa gtt gtc gag gct gac atg      579
82 Gly His Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met
83 175          180          185          190
85 ctc tct aag ggt cta ctc ggt ggc gag gcg tgg tct tcg tgg cat aag      627
86 Leu Ser Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys
87          195          200          205
89 gaa gac tct att cat gta gga gta cgc tgc atc gag atg ctc att gag      675
90 Glu Asp Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu
91          210          215          220
93 tca acc gga atg gtt agc tta cac cgc caa aat gct ggc gta gta ggt      723
94 Ser Thr Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly
95          225          230          235
97 caa gac tct gag act atc gaa ctc gca cct gaa tac gct gag gct atc      771
98 Gln Asp Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile
99          240          245          250
101 gca acc cgt gca ggt gcg ctg gct ggc atc tct ccg atg ttc caa cct      819
102 Ala Thr Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro
103 255          260          265          270
105 tgc gta gtt cct cct aag ccg tgg act ggc att act ggt ggt ggc tat      867
106 Cys Val Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr
107          275          280          285
109 tgg gct aac ggt cgt cgt cct ctg gcg ctg gtg cgt act cac agt aag      915
110 Trp Ala Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys
111          290          295          300
113 aaa gca ctg atg cgc tac gaa gac gtt tac atg cct gag gtg tac aaa      963
114 Lys Ala Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys
115          305          310          315
117 gcg att aac att gcg caa aac acc gca tgg aaa atc aac aag aaa gtc      1011
118 Ala Ile Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val
119          320          325          330
121 cta gcg gtc gcc aac gta atc acc aag tgg aag cat tgt ccg gtc gag      1059
122 Leu Ala Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu
123 335          340          345          350
125 gac atc cct gcg att gag cgt gaa gaa ctc ccg atg aaa ccg gaa gac      1107
126 Asp Ile Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp
127          355          360          365
129 atc gac atg aat cct gag gct ctc acc gcg tgg aaa cgt gct gcc gct      1155
130 Ile Asp Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala
131          370          375          380
133 gct gtg tac cgc aag gac aag gct cgc aag tct cgc cgt atc agc ctt      1203
134 Ala Val Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu

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135	385	390	395	
137	gag ttc atg ctt gag caa gcc aat aag ttt gct aac cat aag gcc atc	1251		
138	Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile			
139	400	405	410	
141	tgg ttc cct tac aac atg gac tgg cgc ggt cgt gtt tac gct gtg tca	1299		
142	Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser			
143	415	420	425	430
145	atg ttc aac ccg caa ggt aac gat atg acc aaa gga ctg ctt acg ctg	1347		
146	Met Phe Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu			
147	435	440	445	
149	gcg aaa ggt aaa cca atc ggt aag gaa ggt tac tac tgg ctg aaa atc	1395		
150	Ala Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile			
151	450	455	460	
153	cac ggt gca aac tgt gcg ggt gtc gat aag gtt ccg ttc cct gag cgc	1443		
154	His Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg			
155	465	470	475	
157	atc aag ttc att gag gaa aac cac gag aac atc atg gct tgc gct aag	1491		
158	Ile Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys			
159	480	485	490	
161	tct cca ctg gag aac act tgg tgg gct gag caa gat tct ccg ttc tgc	1539		
162	Ser Pro Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys			
163	495	500	505	510
165	ttc ctt gcg ttc tgc ttt gag tac gct ggg gta cag cac cac ggc ctg	1587		
166	Phe Leu Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu			
167	515	520	525	
169	agc tat aac tgc tcc ctt ccg ctg gcg ttt gac ggg tct tgc tct ggc	1635		
170	Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly			
171	530	535	540	
173	atc cag cac ttc tcc gcg atg ctc cga gat gag gta ggt ggt cgc gcg	1683		
174	Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala			
175	545	550	555	
177	gtt aac ttg ctt cct agt gaa acc gtt cag gac atc tac ggg att gtt	1731		
178	Val Asn Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val			
179	560	565	570	
181	gct aag aaa gtc aac gag att cta caa gca gac gca atc aat ggg acc	1779		
182	Ala Lys Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr			
183	575	580	585	590
185	gat aac gaa gta gtt acc gtg acc gat gag aac act ggt gaa atc tct	1827		
186	Asp Asn Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser			
187	595	600	605	
189	gag aaa gtc aag ctg ggc act aag gca ctg gct ggt caa tgg ctg gct	1875		
190	Glu Lys Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala			
191	610	615	620	
193	tac ggt gtt act cgc agt gtg act aag cgt tca gtc atg acg ctg gct	1923		
194	Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala			
195	625	630	635	
197	tac ggg tcc aaa gag ttc ggc ttc cgt caa caa gtg ctg gaa gat acc	1971		
198	Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr			
199	640	645	650	

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201 att cag cca gct att gat tcc ggc aag ggt ctg atg ttc act cag ccg      2019
202 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
203 655                               660                               665                               670
205 aat cag gct gct gga tac atg gct aag ctg att tgg gaa tct gtg agc      2067
206 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
207                               675                               680                               685
209 gtg acg gtg gta gct gcg gtt gaa gca atg aac tgg ctt aag tct gct      2115
210 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala
211                               690                               695                               700
213 gct aag ctg ctg gct gct gag gtc aaa gat aag aag act gga gag att      2163
214 Ala Lys Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile
215                               705                               710                               715
217 ctt cgc aag cgt tgc gct gtg cat tgg gta act cct gat ggt ttc cct      2211
218 Leu Arg Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro
219                               720                               725                               730
221 gtg tgg cag gaa tac aag aag cct att cag acg cgc ttg aac ctg atg      2259
222 Val Trp Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met
223 735                               740                               745                               750
225 ttc ctc ggt cag ttc cgc tta cag cct acc att aac acc aac aaa gat      2307
226 Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp
227                               755                               760                               765
229 agc gag att gat gca cac aaa cag gag tct ggt atc gct cct aac ttt      2355
230 Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe
231                               770                               775                               780
233 gta cac agc caa gac ggt agc cac ctt cgt aag act gta gtg tgg gca      2403
234 Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala
235                               785                               790                               795
237 cac gag aag tac gga atc gaa tct ttt gca ctg att cac gac tcc ttc      2451
238 His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe
239                               800                               805                               810
241 ggt acc att ccg gct gac gct gcg aac ctg ttc aaa gca gtg cgc gaa      2499
242 Gly Thr Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu
243 815                               820                               825                               830
245 act atg gtt gac aca tat gag tct tgt gat gta ctg gct gat ttc tac      2547
246 Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr
247                               835                               840                               845
249 gac cag ttc gct gac cag ttg cac gag tct caa ttg gac aaa atg cca      2595
250 Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro
251                               850                               855                               860
253 gca ctt ccg gct aaa ggt aac ttg aac ctc cgt gac atc tta gag tcg      2643
254 Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser
255                               865                               870                               875
257 gac ttc gcg ttc gcg t
258 Asp Phe Ala Phe Ala
259                               880
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 883
264 <212> TYPE: PRT
265 <213> ORGANISM: Bacteriophage T7

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267 <400> SEQUENCE: 2

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268 Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
269 1 5 10 15
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273 20 25 30
276 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
277 35 40 45
280 Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
281 50 55 60
284 Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
285 65 70 75 80
288 Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
289 85 90 95
292 Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
293 100 105 110
296 Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
297 115 120 125
300 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
301 130 135 140
304 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
305 145 150 155 160
308 His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
309 165 170 175
312 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
313 180 185 190
316 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
317 195 200 205
320 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
321 210 215 220
324 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
325 225 230 235 240
328 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
329 245 250 255
332 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
333 260 265 270
336 Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Gly Tyr Trp Ala
337 275 280 285
340 Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
341 290 295 300
344 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
345 305 310 315 320
348 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
349 325 330 335
352 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
353 340 345 350
356 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
357 355 360 365
360 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
361 370 375 380

```

Please Note:

Use f n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequenc Listing t ensure that a c rresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n r Xaa.

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Input Set : A:\024705-077.ST25.txt
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L:1428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1516 M:283 W: Missing Blank Line separator, <220> field identifier
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23